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Minimum DB
Maximum DB
                                                                                                              Post-processing: Minimum Match
Maximum Match
                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                   Database
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                              seq length: 0 seq length: 2000000000
PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 4 3 2 1
                                                                                             Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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3326
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                                                                                                                                                                                                                                                195891 segs, 67900655 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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esult No.	Score	% Query Match	Length DB	₩	ID	Description
	1163		1	2 :	T44430	protein PV100 (imp
2	1112	33.4	566	2	44	in precursor
ω	1074.5			_	FWCNAB	-globulin B
4	1063.5				S06398	ţγ
5	1018.5				S08059	alpha-globulin typ
6	903	•			A53234	globulin-1s, GLB1s
7	m				B53234	vicilin-like stora
- ω	64			N	S35221	1
9	59			_	FWSYBA	beta-conglycinin a
10	858.5				S20007	
11	5.4				B24810	beta-conglycinin a
12	1 8 5 5				S00566	<
14	775 5				706450	62K SHOROSO-bindin
15	759.5				S00567	ilin precurso
16	759.5				S08505	in - garden
17	757.5				S35757	, 4
18	749	•			FWSYCB	
19	740				S24756	vicilin-like stora
20	722	•			S15675	globulin-2 precurs
21	717.5	•			A27288	vicilin precursor
22	713.5	•		2	S06309	
23	712.5	•		Н-	FWPMVB	vicilin B precurso
24	692.5			2	JQ2264	canavalin - jack b
25	685.5	•			S00281	ws -
26	563				A23498	phaseolin type alp
27	560				S10156	alpha-phaseolin pr
28	558.5	•			860190	т.
29	552	•	421		A24810	phaseolin beta cha

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	ω L	30
196	196.5	210	213.5	216	223.5	330	339	356	360	361	365	365	368.5	414	532.5
5.9	5.9	6.3	6.4	б. 5	6.7	9.9	10.2	10.7	10.8	10.9	11.0	11.0	11.1	12.4	16.0
1407	781	551	184	1898	136	481	240	218	407	296	499	196	236	275	540
_	N	Ŋ	ب	1	N	N	Ν	N	N	ν	2	ω	N	بر	Ν
S28589	T02272	S51941	FSFB	A45973	T02870	T14300	T06399	S16334	T02258	T06572	T10443	S02281	T01662	FWPMVA	S21825
trichohyalin - rab	hypothetical prote	prunin 1 precursor	phaseolin - kidney	trichohyalin - hum	globulin 2 precurs	hypothetical prote	7S storage protein	beta-conglycinin a	globulin1 - maize	convicilin precurs	probable major pro	convicilin (clone	globulin-1 - maize	vicilin A precurso	vicilin-like stora

ALIGNMENTS

δÃ δÃ Дb Qy Db Qy В δÃ DЬ δÃ В Qy В Qy A;Molecule type: mRNA A;Residues: 1-810 <YAM> A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1; PID:g3808062 Query Match
Best Local Similarity Matches 271; 322 AKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVLGQQRE--GV 379 446 326 167 LQYQCQRRCQEQ------QRQHGRGG-------DLMNPQRGGSGRYEE-----GEEK 205 266 133 211 154 GRGRRDENERDPKREQEERQR--REQERRREQEQRERERRGERDEEDDEN-QRDPDWRR 86 32 94 10 QMRRCVSQCDKRFEE------DIDWSKY------VKLVQPVNNPGEFKDYLSAGGES-QAYYSVFSNDVLEAALNIPRDKLERIFKQRRERGGK 563 REQERRRREEEQREREWEREHGRRGREEQRSREDERRRHERQHGGRSRVNQVAIRRTEQE 385 EKYEERMKEGDNKRDP------QQREYEDCRRHCEQQ--------Ep--R 166 EQ-----ERREQERRRREQEQERRERQRRGGRDDEDENQRDPDWRREQKRREQEGERRER 265 LDADAILLVIGGRGALKMIHRDNR----ESYNLECGDVIRIPAGTTFYLINRDNNERLHI 321 ERRGGRDDEDENQRDPDWRREQERREQERRREREQERREREHRGGRDVEDENQRDPDWR -----DNQEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEEEYNRQRDPQQQY 85 QQRKCEQVCEERLREREQGRGEDVDEVERRDPEWEREEQRRREHEREERRRRERERERER LDAECVLLVVRGRATITTVVQEKRETRKESYNVESGDVMTIPAGTTLYLANQE-NEDLQI 504 EQCQKRCQRRETEPRHMQICQQRCERRY------EKE-----KRKQQKRYEEQQREDE 132 Conservative 133; Mismatches 192; 35.0%; Score 1163; DB 2; 36.8%; Pred. No. 6.1e-66; 2 Length 810; Indels 140; Gaps 325 210 153 31 22;

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vicilin precursor - cacao (C.Species: Theobroma cacao (Cacao) (C.Species: Theobroma cacao (Cacao) (C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change C:Accession: $22477; $22478; $18105; $22050 C:Accession: $22477; $22478; $18105; $22050 Pint Mol. Biol. 18, 1173-1176, 1992 A:Reference number: $22477; MUID:92288309 A:Accession: $22477; MUID:92288309
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A; Residues: 1-452 < MC2>
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A;Accession: S22478
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  362 NTQTERLRGVLGQQR--
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nes 234; Conserv
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                                                                                                                      VPAGSTVYVVSQDNQEKLTIAVLALPVNSPGKYELFFPAGNNKPESYYGAFSYEVLETVF
                                                                                                                                             LRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIR 301
                                                                                                                                                                                                                            GRGGDLMNPQRGGSGRYEEGEEKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSKL
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                                                                              IPAGTTFYLINRDNNERLHIAKFLOTISTPGQYKEFFPAGGONPEPYLSTFSKEILEAAL
                                                                                                                                                                                                     ER-GEHENYHNHKKNRSEEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPP 175
                                                                                                                                                                                                                                                                                    KEQQRQQEEEL
                                                                                                                                                                                                                                                                                                                       EEQQREDEEKYEERMKEGDNKRDPQQREYEDCRRHCEQQE--PRLQYQCQRRCQEQQRQH 182
                                                                                                                                                                                                                                                                                                                                                               LCSGVSAYGRKQYERDPRQQYEQCQRRCESEATEEREQEQCEQRCER------EY
                                                                                                                                                                                                                                                                                                                                                                                                      ICEEEEEYNR----QRDPQQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRY 124
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    -EGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGP
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C;Comment: This is a seed storage protein.
C;Superfamily: 91ycinin
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A; Residues: 1-81 <CH2>
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A; Accession: S06911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-588 < CHL>
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R;Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III,
Plant Mol. Biol. 7, 475-489, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-globulin B precursor (clone C72) - upland cotton
N;Alternate names: seed storage protein; vicilin precursor
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 229; Conserv
    265
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HLDADAILLYIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKF
                                     EQSHNPFHFHRRSFQSRFREEHGNFRVLQRFASRHPILRGINEFRLSILEANPNTFVLPH
                                                              KQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVLPT
                                                                                                                                                                                                                                        QRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEGDNKRDPQQRE 152
                                                                                                                                                                                                                                                                                                                     EDPOTECOOCORRCROQESDPROQOYCORRCKEICEEEEEYNROR--DPOOQYEOCOKRC
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RESULT 4

$06398

alpha-globulin type A precursor - upland cotton
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: $06398
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination
A;Reference number: $06398
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-605 <CHL>
C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted <MAT>
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PHLPRQSSYEEEEEEDEEEEQEQEEEERRSGQYRKIRSRLSRGDIFVVPANFPVTFVASQN
                                                                                              NQNGRFFEACPPEFRQLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTEGNGYAEMVS
                                                                                                                                                NKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMAC
                                                                                                                                                                                                  FGGROSRRROQGOGMFRKASOEQIRALSQEATSPR----EKSGE--RFAFNLLSQTPRYS
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A;Residues: 1-573 <BEL>
A;Residues: 1-573 <BEL>
A;Experimental source: inbred line Va 26
A;Note: sequence extracted from NCBI backbone (NCBIN:71280, NCBIP:71284)
R;Kriz, A.L.
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Genetics 129, 863-872, 1991
A;Title: Molecular basis for allelic polymorphism
A;Reference number: A53234; MUID:92090707
A;Accession: A53234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   globulin-15, GLBIS - maize
C;Species: Zea mays (maize)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C;Accession: A53234; A43642
R;Belanger, F.C.; Kriz, A.L.
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A;Title: Characterization of embryo globulins encoded A;Reference number: A43642; MUID:89374022
A;Accession: A43642
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HRQSQGGESERERGKGRRSEEEEESSEEQEEVGQGYHTIRARLSPGTAFVVPAGHPFVAV
                                 HLSGRHG----GRGGGKRHEEEEEVHYEQ-----VRARLSKREAIVVLAGHPVVFV 532
                                                                          QHGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLYNTRSFKIAYVPNGKGYAEIVCP
                                                                                                           KYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP 485
                                                                                                                                                                                                                          ANTDGRKKLVITKILHTISVPGEFQFFFGPGGRNPESFLSSFSKSIQRAAYKTSSDRLER 263
                                                                                                                                                                                                                                               INRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRG
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37.2%;
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Pred. No. 1e-49;
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C;Species: Zea mays (maize)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: B53234, S21824
R;Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A;Title: Molecular basis for allelic polymorphism of the maize
A;Reference number: A53234; MUID:92090707
A;Accession: B53234
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A; Residues: 1-582 <BEL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X59083; NID:g22283; PIDN:CAA41809.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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Best Local Similarity
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                                                                                                                                                                                                                                     261 LFGRHGQDKGIIVRATEEQTRELRRHASEGGHGPHWPLPPFGE-SRGPYSLLDQRPSIAN
                                                                                                                                                                                                                                                                                                                                                     311 INRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRG
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                    VSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQD
                                                                                                                                                                             KYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP 485
                                                                                                                                                                                                                                                                                                            ANTDGRKKLVITKILHTISVPGEFQFFFGPGGRNPESFLSSESKSIQRAAVKTSSDRLER
                                                                                                                                                                                                                                                                                                                                                                                                                    VLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEYNRQRDPQQQYEQCQKRCQRRETEPRHMQ-ICQQRCERRYEKEKRKQQKRYEEQQRED
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VASRDSNLQTVCFEVHADRNEKVFLAGAD-NVLQKLDRVAKALSFASKAEEVDEVLGSRR
                                                                                                                                                       QHGQLYEADARSFHDLAEHDVSVSFANITAGSMSAPLFNTRSFKIAYVPNGKGYAEIVCP
                                                                                                                                                                                                                                                                           VLGQ--QREGVIIRASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLFNKRPLYSN 425
                                                                                                                                                                                                                                                                                                                                                                                            AVLEANPRSFVVPSHTDAHCICYVAEGEGVVTTIENGERRSYTIKQGHVFVAPAGAVTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRGGSGRYEEGEEKQSD-NPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGFLPGPKESGGHEEREQEEEEREE
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                                                                           HRQSQGGESERERDKGRRSEEEEEESSEEQEEAGQGYHTIRARLSPGTAFVVPAGHPFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KEKQKDRRPYVFDRRSFRRVVRSEQGSLRVLRPFDEVSRLLRGIRDYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGSSED------EREQE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEKYEERMKEGDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNP 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDDNIIHHHGGIIKSGQCVRRCEDR----PWHQRPRCLEQC-REEEREKRQERSRHEADDRSG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASRDSNLQIVCFEVHADRNEKVFLAGAD-NVLQKLDRVAKALSFASKAEEVDEVLGSRRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 888; DB 2;
Pred. No. 9.4e-49;
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                                                                                                                --YEQVRARLSKREAIVVLAGHPVVF 531
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globulin Beg1 precur
C;Species: Hordeum v
C;Date: 03-Feb-1994
C;Accession: S35221
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A;Map position: 4
A;Map position: 4
C;Superfamily: glycinin
C;Keywords: glycoprotein
E;174-190/Product: globulin Beg1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Heck, G.R.; Chamberlain, A.K.; Ho, T.H.; Mol. Gen. Genet. 239, 209-218, 1993
A:Title: Barley embryo globulin 1 gene, But Reference number: S35221; MUID:93287988
A:Accession: S35221
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A:Residues: 1-637 <HEC>
A:Cross-references: EMBL:M64372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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| Species: Hordeum vulgare (barley)
| Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 221; Conserv
                                                                                                                                                               405
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               585
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ELFNSQDESI-FFPGPRQHQQQSPRSTKQQQ
                                                                                                                                                                             AYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHL---
                                         HPVVEISSSQGSSNLQVVCFEINAERNERVWLAGR-NNVIGKLGSPAQELTFGRPAREVQ
                                                                     HPVVFVSS--GNENLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVE
                                                                                                   ESESEREHGKGRRREEEEDDQRQQRRRGSESESEEEEEQQRYETVRARVSRGSAFVVPPG
                                                                                                                                                            LYEADARSFHALANQDVRVAVANITPGSMTAPYLNTQSFKLAVVLEGEGEVQIVCPHLGR
                                                                                                                                                                                                                     EKTRSVSIVRASEEQLRELRREAAEGGQGHRWPLPPFRGDSRDTFNLLEQRPKIANRHGR
                                                                                                                                                                                                                                     ---REGVIIRASQEQIRELTRDDSE---SRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQ 429
                                                                                                                                                                                                                                                                                LVIAKILHTISVPGKF-QFL----SVKPLLASLSKRVLRAAFKTSDERLERLFNQRQGQ
                                                                                                                                                                                                                                                                                                            LHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVLGQQ---
                                                                                                                                                                                                                                                                                                                                          AFVVPGFTDADGVGYVAQGEGVLTVIENGEKRSYTVKEGDVIVAPAGSIMHLANTDGRRK
                                                                                                                                                                                                                                                                                                                                                                      AFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNER
                                                                                                                                                                                                                                                                                                                                                                                                   ERDEEQGDSRRPYVFGPRSFRRIIQSDHGFVRALRPFDQVSRLLRGIRDYRVAIMEVNPR
                                                                                                                                                                                                                                                                                                                                                                                                                               E--EKQSDN--PYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEGEREEERGRGHGRHGEGE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRG----GDLMNPQRGGSGRYEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERMKEGDNKR 146
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Pred. No. 3.2e-47;
0; Mismatches 219;
                                                                                                                               --GGKRHEEEEEVHYEQVRARLSKREAIVVLAG
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Best Local Similarity
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            EGDANIELV -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133;
          -GLKEQQQEQQQEEQPLEVRKYRAELSEQDIFVIPAGYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
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C: Keywords: glycoprotein; seed; storage protein F;1-22/Domain: signal sequence #status predicted <SIG>F;23-62/Domain: propeptide #status predicted <PRO>F;63-605/Product: beta-conglycinin alpha chain #status predict F;261,517/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 189-196,'H',198,'N',200,'X',202-203;397-408,'X',410,'X',412-417,'X',419-4 A; Experimental source: seed C; Superfamily: glycinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;ACCESSION TYPE: mRNA
A;Residues: 1-605 <SEB>
A;Cross references: EMBL:X17698; NID:g18535; PIDN:CAA35691.1;
A;Cross references: EMBL:X17698; NID:g18535; PIDN:CAA35691.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-conglycinin alpha chain precursor - soybean C; Species: Glycine max (soybean) C: Date: 31-Dec:1991 #sequence_revision 31-Dec:1991 #text_change C; Accession: $14681; $74124; $06714 R; Sebastian1, F.L.; Farrell, L.B.; Schuler, M.A.; Beachy, R.N. Plant Mol. Biol. 15, 197-201, 1990 A; Title: Complete sequence of a cDNA of alpha subunit of soybean A; Reference number: $14681; MUID:91355860
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Eur. J. Biochem. 241, 221-228, 1996
A;Title: Limited proteolysis of beta-conglycinin and glycinin, A;Reference number: S74123; MUID:97054613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAG
SGEADVEMACPHLSGRHGGRGGGKRHEEEEEVHYEQ-----VRARLSKREAIVVLAGHP 528
                                                                                                                NLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVA 474
                                                                                                                                                                                                  EEINKVLFSREEGQQQGEQRLQESVIVEISKEQIRALSKRAKSSSRKTI----SSEDKPF
                                                                                                                                                                                                                                                                                                                            TTYYVVNPDNNENLRLITLAIPVNKPGRFESFFLSSTEAQQSYLQGFSRNILEASYDTKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDNQEDPQTECQQCQRRCRQQESDPRQQQYCQRRC----KEICEEEE-----EYNR
                                                                NLRSRDPIYSNKLGKFFEITPEKNPQLRDLDIFLSIVDMNEGALLLPHFNSKAIVILVIN
                                                                                                                                                                                                                                                           ERLRGVL------GQQR--EGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPY 414
                                                                                                                                                                                                                                                                                                                                                                                         TTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDYRILEFNSKPNTLLLPNHADADYLIVILNGTAILSLVNNDDRDSYRLQSGDALRVPSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQRGGSGRYEEGEEKQ-----SDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - EESEDSELRRHKNKNPFLFGSNRFETLFKNQYGRIRVLQRFNQRSPQLQNL
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No. 6.2e-47;
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V.P.; Horstmann,
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beta-conglycinin alpha chain precursor - soybean
C:Species: Glycine max (soybean)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-C:Accession: $20007
R:Lelievre, J.M.; Dickinson, C.D.; Dickinson, L.A.; Nielsen, N.C. Plant Mol. Biol. 18, 259-274, 1992
A:Title: Synthesis and assembly of soybean beta-conglycinin in vitro A:Reference number: $20007; MUID:92119248
A:Accession: $20007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-605 <LEL>
C:Superfamily: glycinin
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                                                                                                   LLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQDESIFFPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQDESIFFPGPRQHQQQSPRSTKQQQPLVSIL 620
PKKKEEGNKGRK--GPLSSIL
                                                                                                                                                                                        HLSGRHGGRGGKRHEEEEEVHYEQ------VRARLSKREAIVVLAGHPVVFVSSGNENL
                                                                                                                                                                                                                                                                                                                                                                                                                                      ERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTERLRGVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEDSELRRHKNKNPFLFGSNRFETLFKNQYGRIRVLQRFNQRSPQLQNLRDYRILEENSK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEEKQ-----SDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEE
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                                      RQHQQQSPRSTKQQQPLVSIL
                                                                              NFFAIGINAENNQRNFLAGSQDNVISQIPSQVQELAFPGSAQAVEKLLKNQRESYFVDAQ
                                                                                                                                                                                                                                                KLGKFFEITPEKNPQLRDLDIFLSIVDMNEGALLLPHFNSKAIVILVINEGDANIELV--
                                                                                                                                                                                                                                                                                    KYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACP 485
                                                                                                                                                                                                                                                                                                                              EGQQQGEQRLQESVIVEISKEQIRALSKRAKSSSRKTI----SSEDKPFNLRSRDPIYSN
                                                                                                                                                                                                                                                                                                                                                        -----GQQR--EGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSN 425
                                                                                                                                                                                                                                                                                                                                                                                                             ENLRLITLAIPVNKPGRFESFFLSSTEAQQSYLQGFSRNILEASYDTKFEEINKVLFSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNTLLLPNHADADYLIVILNGTAILSLVNNDDRDSYRLQSGDALRVPSGTTYYVVNPDNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YWEKENPKH -- NKCLQSC - NSERDSYRNQACHARCNLLKVEKEECEEGEIPRPRPRPRPQHP
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                                                                                                                                                               GLKEQQQEQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVV--NATSNL
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A;Cross-references: GB:M13759; NID:g169928; PIDN:AAB01374.1; PID:g169929 A;Note: the authors translated the codon GGT for residue 352 as Glu R;Schuler, M.A.; Schmitt, E.S.; Beachy, R.N. Nucleic Acids Res. 10, 8225-8244, 1982 A;Title: Closely related families of genes code for the alpha and alpha' subunits A;Reference number: S16337; MUID:83143288 A;Accession: S16337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Doyle, J.J.; Schuler, M.A.; Godette, W.D.; Zenger, V.; Beachy, R.N.; Slightom, J. Biol. Chem. 261, 9228-9238, 1986
A;Title: The glycosylated seed storage proteins of Glycine max and Phaseolus vul. A;Reference number: A24810; MUID:86250867
A;Accession: B24810; MUID:86250867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues:
C; Genetics:
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A; Residues: 1-639 < DOY>
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                           IVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASR 580
                                                                                                                               FFNTRSTKVVVVAASGEADVEMACPHLSGRHGGRGGGKRHEEEEEE-VHYEQVRARLSKREA
                                                                                                                                                                                                                                          HIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGP
                                                                                                                                                                                                                                                                                                                                                                                                                    LLEANPNAFYLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIP------
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                                                                                              HENSKAIVVLVINEGEANIELV------GIKEQQQRQQQEEQPLEVRKYRAELSEQDI
                                                                                                                                                                                                TI----SSEDKPFNLGSRDPIYSNKLGKLFEITQRN-PQLRDLDVFLSVVDMNEGALFLP
                                                                                                                                                                                                                                                                                            SKNILEASYDTKFEEINKVLFGREEGQQQGEERLQESVIVEISKKQIRELSKHAKSSSRK
                                                                                                                                                                                                                                                                                                                                         SKEILEAALNTQTERLRGVL ----- GQQ ----- REGVIIRASQEQIRELTRDDSESRRW 401
                                                                                                                                                                                                                                                                                                                                                                                         NPDNDENLRMTAGTTFYVVNPDNDENLRMITLAIPVNKPGRFESFFLSSTQAQQSYLQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFNSKPNTLLLPHHADADYLIVILNGTAILTLVNNDDRDSYNLQSGDALRVPAGTTFYVV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESEGSESQREPRRHKNKNPFHFNSKRFQTLFKNQYGHVRVLQRFNKRSQQLQNLRDYRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRGGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEQDER--EHPRPHQPHQKEEE---KH-EWQHKQEKHQGKESEEEEEDQDEDEEQDKESQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKYEERMKEGDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQ-HGRGGDLMNP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEKQNPSHN-----KCLRSC-NSEKDSYRNQACHARCNLLKVEEEEEECEEGQIPRPRPQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 141;
-NATSDLNFFAFGINAENNQRNFLAGSKDNVISQIPSQVQELAFPRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.7%; Score 854.5; DB 2; 32.0%; Pred. No. 1.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                             461
                                                                                                                                                                                                                                                                                                                                                                                         372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303
597
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B

487

NLNLL--GFGINAKNNQRNFLSGSDDNVISQIENPVKELTFPGSSQEVNRLIKNQKQSHF 544

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A:Map position: 2
A:Introns: 221/1; 279/3; 304/3; 412/3; 507/1
C:Superfamily: glycinin
F:1-28/Domain: signal sequence #status predicted
F:29-571/Product: convictiin #status
                                                                                                                     B
                                                                                                                                                     QУ
                                                                                                                                                                                           DЬ
                                                                                                                                                                                                                       Qγ
                   20
                                                       Вþ
                                                                                   Qy
                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                           Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Cross-references: EMBL:X06398; NID:g20698; PIDN:CAA29695.1; PID:g313670 A;Note: part of this sequence, including the amino end of the mature protein, A;Note: 237-Gln was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Bown, D.; Ellis, T.H.N.; Gatehouse, J.A
Biochem. J. 251, 717-726, 1988
A;Title: The sequence of a gene encoding
A;Reference number: S00566; MUID:88326208
A;Accession: S00566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            convicilin precursor (clone pJC4) - g
C; Species: Pisum sativum (garden pea)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: 237
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-571 <BOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Date: 30-Jun-1989 #sequence_revision C:Accession: S00566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: cvcA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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Best Local S
Matches 208
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                     536
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les 208; Conserv
NENLLLFAFGINAONNHENFLAGRERNVLOQIEPQAMELAFAASRKEVEELFNSQDESIF
                                                                                                                                                                                                                                                                           LPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHI 321
                                                                                     MACPHLSGRHGGRGGGKRHEEEEEVHYE----
                                                                                                                       YSNKFGKLFEITPEKKYPQLQDLDILVSCVEINKGALMLPHYNSRAIVVLLVNEGKGNLE
                                                                                                                                              YSNKYGQAYEVKPE-DYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVE
                                                                                                                                                                                         QLRDRKRTQQGEERD-AIIKVSREQIEELRKLAKSSS----KKSLPSEFEPFNLRSHKPE
                                                                                                                                                                                                                                                           VDFVIPVNRPGKFEAF -- GLSENKNQYLRGFSKNILEASLNTKYETIEKVLLEEQEKKPQ
                                                                                                                                                                                                                                                                                                                                                                                               SESQEHRNPFLFKSNKFLTLFENENGHIRRLQRFDKRSDLFENLQNYRLVEYRAKPHTIF
                                                                                                                                                                                                                                                                                                                                                                                                                               GEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQRREDPEER------ARLRHREER--TKRDRRH------QREGEEEERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQHGRGGDLMNPQRGGSGRYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTYANYD - - EGSETRVPGQRERGRQ
                                                                                                                                                                                                                                                                                                                             LPQHIDADLILVVLNGKAILTVLSPNDRNSYNLERGDTIKIPAGTTSYLVNQDDEEDLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E-----KEEHE-----EEKQKYRYQREKKEQKEVQPGRERWEREEDEEQVEEEWRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQK----RYEEQQREDEEKYEERMKE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDWSKYDNQEDPQTECQQCQRRCRQQESDPRQQQYCQRRCKEICEEEEEYNRQRDPQQQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDIENLIKSQSESYFVDA--QPQQKEEGNKGRKGPLSSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                   -----GLKNEQQEREDRKERNNEVQRYEARLSPGDVVIIPAGHPVAISASS
                                                                                                                                                                                                                         -GQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gatehouse, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 833; DB 2;
Pred. No. 2.7e-45;
2; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            garden
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                                                                          -QVRARLSKREAIVVLAGHPVVFVSSG
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Qγ
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A;Rosidues: 1-524 <GRI>
A;Cross-references: GB:L06038; NID:g1431744; PIDN:AABO:C;Superfamily: g1ycinin
C;Keywords: sugar transport
F;1-29/Domain: signal sequence #status predicted <SIG>F;30-524/Product: 62K sucrose-binding protein #status;
                                                                                                                                          B
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A;Title: A 62-kD sucrose binding protein is expressed and localized A;Reference number: JQ1730; MUID:93104680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62K sucrose-binding protein precursor - C; Species: Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
JQ1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JQ1730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
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Best Local Similarity
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491
                                   582
                                                                    432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 RCKEICEEEEEYNRQRDPQ--QQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQ 121
LIGRLYHLPHKDRKESFFFFFELPREERGRRA
                               EVEELFN----SQDESIFFPGPRQHQQQSPRS
                                                                                                                                                                                                                             KRPLYSNKYGQAYEVKPEDYRQ--LQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASG
                                                                                                                                                                                                                                                                                                       AALNTQTERLRGVLGQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFN
                                                                                                                                                                                                                                                                                                                                                      HIPAGTPLYIVNRDENDKLFLAMLHIPVSVSTPGKFEEFFAPGGRDPESVLSAFSWNVLQ
                                                                                                                                                                                                                                                                                                                                                                              RIPAGTTFYLINRDNNERLHIA--KFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGRGGDLMNPQRGGSGRYEEGEEKQSDNPYYFDE-RSLSTRFRTEEGHISVLENFYGRSK 240
                                                                                                   ENLLLFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAF----
                                                                                                                                      RGHLQISCPHMS----SRSSHSKHDKSSP-SYHRISSDLKPGMVFVVPPGHPFVTIASNK
                                                                                                                                                                        EADVEMACPHLSGRHGGRGGGKRHEEEEEVHYEQVRARLSKREAIVVLAGHPVVFVSSGN
                                                                                                                                                                                                           KRPTISNGYGRLTEVGPDDDEKSWLQRLNLMLTFTNITQRSMSTIHYNSHATKIALVIDG
                                                                                                                                                                                                                                                                               AALQTPKGKLENVFDQQNEGSIFRISREQVRALA-PTKKSSWWPF--GGE-SKPQFNIFS
                                                                                                                                                                                                                                                                                                                                                                                                                        LLQGIENFRLAILEARAHTFVSPRHFDSEVVFFNIKGRAVLGLVSESETEKITLEPGDMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H-----EEQDENPYIFEEDKDFETRVETEGGRIRVLKKFTEKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRYEEQQREDEEKYEERMKEGDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQRQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCKETEVEEE-----DPELVTCKHQCQOOQQYTEGDKR---VCLQSCD-RYHRMKQERE 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KKEEESRERE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 794; DB 2;
Pred. No. 7.1e-43;
3; Mismatches 176
                                                                  NIVSSLDNVAKELAFNYPSEMVNGVFLLQRFLERK
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522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 524;
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                                                                                                   --AASRK 581
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                                                                                                                                     431
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14

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vicilin precursor (clone pDUB9) - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
C:Accession: S00567
R:Watson, M.D.; Lambert, N.; Delauney, A.; Yarwood, J.N.; Croy, R.R.D.; Gate
Biochem. J. 251, 857-864, 1988
                                                                                                                 RESULT
S00567
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62K sucrose-binding protein homolog - garden pea
N:Alternate names: P54 protein
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06459
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C:Genetics:
A:Note: p54
C:Superfamily: glycinin
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A:Accession: T00459
A:Status: preliminary; translated from A:Molecule type: mRNA
A:Residues: 1-483 <ROD>
A:Cross-references: EMBL:Y11207; PIDN:C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYLSTFSKEILEAALNTQTERLRGVLGQQREGVIIRASQEQIRELTRDDSESRRWHIRRG
                                                                                                                                                                                              VFERKEE-FFFPYDNEERKE
                                                                                                                                                                                                                                 LFNSQDESIFFPGPRQHQQQ 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERFNLEEGDIMRVPAGTPMYLVNRDENEKLYIAAFHMPPSSGSAPVNLEPFFESAGRKPE
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                                                                                                                                                                                                                                                                            GHPFVNIASKKKNLIVVCFEVNAQRNKKLALAGK-KNIVSALDKAAKEVAFDIAAEKVDE
                                                                                                                                                                                                                                                                                                                                                     NANKIALVIDGEGELEMACPHMPS----SSSNSRQKKSSISYHNINAKLRPGVMFVVPA
                                                                                                                                                                                                                                                                                                                                                                                           RSTKVVVVASGEADVEMACPHLSGRHGGRGGGKRHEEEEEEVHYEQVRARLSKREAIVVLA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPFKSPFNIFSNNPAFSNKFGSLFEVGPSQEKSGLEGLNLMLTLANTTKGSMSTIHYNT
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                    Croy, R.R.D.; Gatehouse,
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F;1-Z/Domain: signal sequence (fragment) #status predicted
F;3-433/Product: vicilin #status predicted <MAT>
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A;Acession: $00567
A;MOlecule type: mRNA
A;Residues: 1-433 <WAT>
A;Cross-references: EMBL:Y00722; NID:920915; PIDN:CAA68708.1; PID:9758248
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                                                                                   AFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQDESIFFPGPRQH
                                                                                                                                                                                                               DAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERLHIAKFLQTI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPFIFKSNKFQTLFENENGHIRLLQKFDQRSKIFENLQNYRLLEYKSKPHTIFLPQHTDA
                                                               GFGINAENNQRNFLAGDEDNVISQVQRPVKELAFPGSAQEVDRILENQKQSHFADAQPQQ
                                                                                                                                                    RHGGRGGGKRHEEEEEEVHYEQV-----RARLSKREAIVVLAGHPVVFVSSGNENLLLF
                                                                                                                                                                                                FFEITPEKNPQLQDLDIFVNSVEIKEGSLLLPHYNSRAIVIVTVNEGKGDFELVGQRNEN
                                                                                                                                                                                                                                                                                          ---GQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQ 429
                                                                                                                                                                                                                                                                                                                            NRPGQLQSFLLSGNQNQQNYLSGFSKNILEASFNTDYEEIEKVLLEEHEKETQHRRSLKD 187
                                                                                                                                                                                                                                                                                                                                                                                            DYILVVLSGKAILTVLKPDDRNSFNLERGDTIKLPAGTIAYLVNRDDNEELRVLDLAIPV 127
RERGSRETRDR 429
                              QQQSPRSTKQQ 613
                                                                                                                                                                                                                                                             KRQQSQEENVIVKLSRGQIEELSKNAKSTS----KKSVSSESEPFNLRSRGPIYSNEFGK
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                                                                                                                               -KEDDEEEEQGEEEINKQVQNYKAKLSSGDVFVIPAGHPVALKASSNLDLL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 759.5; DB 2
Pred. No. 8.5e-41;
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Search completed: March 1, 2001, 15:52:36 Job time: 560 sec